View metadata, citation and similar papers at core.ac.uk
brought to you by CORE
provided by Elsevier - Publisher Connector

plays a conserved role as a homeotic regulator, during vertebrate development.

doi:10.1016/j.ydbio.2010.05.397

Program/Abstract # 417
Integrative imaging of the developing opossum cochlea
Lisa Noelle Cooper, Karen E. Sears
Department of Animal Bio., Univ. of Illinois, Urbana, IL 61801, USA

The short-tailed opossum (*Monodelphis domestica*) is a marsupial mammal that gives birth to highly underdeveloped young that complete much of their sensory development outside the womb while fused to the mother's teat. While suckling, the primary organ of hearing, the cochlea, undergoes an extraordinary morphological transition from a cylinder to a coiled cochlea with 1.9 turns. Because this transition occurs *ex utero*, opossum cochlear development can be experimentally manipulated *in vivo*, making the opossum an ideal model for inner ear development. This is important, as the genetic underpinnings of cochlear morphogenesis are largely unknown. This study utilizes the opossum as a novel mammalian model for cochlear development, with the aim of synthesizing developmental morphogenetic and molecular signaling data to pinpoint mechanisms shaping mammalian cochlear development. High resolution computed tomography (CT) and magnetic resonance imaging (MRI) technologies allowed visualization of cochlear outgrowth and coiling. Comparisons with histological sections and cleared and stained pups indicated that MRI scans more accurately differentiated soft tissue boundaries, and these data were used to reconstruct a 3D model of opossum cochlear development. Central toward understanding cochlear outgrowth is pinpointing regions of cell proliferation and apoptosis. Apoptosis assays indicated that cell death occurred along the base of the developing cochlear coils, while proliferation (phosphohistone-H3) preferentially occurred along their lateral margins. Taken together, these results lay the foundation for future utilization of the opossum as a novel model for mammalian inner ear morphogenesis.

doi:10.1016/j.ydbio.2010.05.398

Program/Abstract # 418
A new model for the evolution of the vertebrate jaw
Daniel M. Medeiros[a], Jacob Doherty[a], Maria V. Cattell[a], Tatjana Sauka-Spengler[b], Marianne Bronner-Fraser[b], Feiqiao Yu[b], Robert Cerny[c]
[a]*EBIO Department, Univ. of Colorado, Boulder, CO, USA*
[b]*Div. of Biol., CALTECH, Pasadena, CA, USA*
[c]*Department of Zool., Charles University in Prague, Czech Republic*

The appearance of jaws was a turning point in vertebrate evolution because it allowed primitive vertebrates to capture and process large, motile prey. The vertebrate jaw consists of separate dorsal and ventral skeletal elements connected by a joint. How this structure evolved from the unjointed gill bars of a jawless ancestor is an unresolved question in vertebrate evolution. To understand the developmental bases of this evolutionary transition, we examined the expression of 12 genes involved in vertebrate pharyngeal patterning in the jawless fish, lamprey. Contrary to previous reports, we find nested expression of *Dlx* genes, and combinatorial expression of *Msx*, *Hand* and *Gsc* genes along the dorso-ventral (DV) axis of the lamprey pharynx, indicating gnathostome-type pharyngeal patterning evolved before the appearance of the jaw. In addition, we find that Bapx and Gdf5, key regulators of joint formation in gnathostomes, are not expressed in the lamprey first arch, while Barx, which is absent from the intermediate first arch in gnathostomes, marks this domain in lamprey. Taken together, these data support a new scenario for jaw evolution in which recruitment of Bapx and Gdf5 into a pre-existing DV patterning program drove the evolution of the jaw by altering the identity of intermediate first arch chondrocytes. We present this "Pre-pattern/Cooption" model as an alternative to current models linking the evolution of the jaw to the evolution of novel pharyngeal DV pattern.

doi:10.1016/j.ydbio.2010.05.399

Program/Abstract # 419
The role of neural crest progenitor population specification and proliferation dynamics in establishing species-specific differences in jaw size
Jennifer L. Fish, Rich A. Schneider
Department of Orthopaedic Surgery, University of California at San Francisco, San Francisco, CA, USA

The diversification and adaptive success of vertebrates owes a great deal to their specialized feeding apparatuses. The jaw skeleton derives from the cranial neural crest (CNC), a population of cells unique to vertebrates. Despite its basic developmental conservation, the adult jaw varies tremendously in both size and shape. Recently, the orchestration of developmental programs regulating jaw size and shape has been shown to be under the control of CNC cells. Yet, underlying molecular and cellular mechanisms driving species-specific changes in jaw size remain unknown. To test the hypothesis that CNC progenitor population number and proliferation rates contribute to species-specific differences in jaw size, we compare CNC development in two morphologically distinct birds, duck and quail. We analyze expression of genes involved in neural tube regionalization including *Otx2*, *Foxg1*, *Fgf8*, and *Krox20*, and genes involved in the induction and maintenance of CNC such as *Pax7*, *FoxD3*, and *Sox10*, in duck and quail embryos at Hamburger and Hamilton (HH) stages 4–12. These stages span the period of time when CNC become specified and emigrate from the rostral neural tube. We also compare proliferation rates in duck and quail premigratory CNC and postmigratory mandibular mesenchyme, which show that duck CNC proliferate more slowly than those of quail. Our results indicate that molecular and cellular differences emerge early on during duck and quail development, which likely contribute to species-specific variation in jaw size.

doi:10.1016/j.ydbio.2010.05.400

Program/Abstract # 420
Evolution of vertebrate skeletal myogenesis: Insights from the cyclostome lamprey
Rie Kusakabe[a,b], Shigehiro Kuraku[c], Shigeru Kuratani[b]
[a]*Department of Biol., Grad. Sch. Sci., Kobe Univ., Japan*
[b]*Lab. for Evol Morph., CDB, RIKEN, Japan*
[c]*Dept. Biol., Univ. of Konstanz, Germany*

Skeletal muscles of gnathostomes (jawed vertebrates) are categorized into epaxial and hypaxial groups morphologically separated at the level of the notochord. During development, portions of the hypaxial dermomyotome undergo delamination to provide migratory myoblasts that give rise to the tongue muscles, the tranpezius (cucullaris) muscles, and the limb muscles. These muscles require activation of specific developmental genes, such as MRFs, Pax3 and Lbx1, at the ventral (hypaxial) side of the dermomyotome. To gain